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TECH CENTER 1600/2900

1633

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/771,045A

DATE: 05/03/2001
 TIME: 12:58:01

Input Set : A:\1134CSEQLIST.TXT
 Output Set: N:\CRF3\05032001\I771045A.raw

ENTERED

4 <110> APPLICANT: Duvick, Jonathan P.
 5 Gilliam, Jacob T.
 6 Maddox, Joyce R.
 8 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
 9 Polynucleotides and Related Polypeptides and Methods of Use
 12 <130> FILE REFERENCE: 1134C
 14 <140> CURRENT APPLICATION NUMBER: 09/771,045A
 15 <141> CURRENT FILING DATE: 2001-01-26
 17 <150> PRIOR APPLICATION NUMBER: US 60/092,936
 18 <151> PRIOR FILING DATE: 1998-07-15
 20 <150> PRIOR APPLICATION NUMBER: US 60/135,391
 21 <151> PRIOR FILING DATE: 1999-05-21
 23 <150> PRIOR APPLICATION NUMBER: US 09/352,159
 24 <151> PRIOR FILING DATE: 1999-07-12
 26 <150> PRIOR APPLICATION NUMBER: US 09/352,168
 27 <151> PRIOR FILING DATE: 1999-07-12
 29 <160> NUMBER OF SEQ ID NOS: 53
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 34 <211> LENGTH: 372
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Exophiala spinifera
 38 <220> FEATURE:
 39 <221> NAME/KEY: misc_feature
 40 <222> LOCATION: (346)...(346)
 41 <223> OTHER INFORMATION: n = A,T,C or G
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 45 gcttgactg ttgggaccac ttccgtccc ggtctccgac catgaaacag gtaatggacc 120
 46 attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt 180
 47 ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct 240
 48 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg 300
 49 gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc 360
 50 ggaacacggc gc 372
 52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 182
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Exophiala spinifera
 57 <400> SEQUENCE: 2
 58 gaattttccg ccaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caaggtggga 60
 59 tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc 120
 60 gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180
 61 ac 182
 63 <210> SEQ ID NO: 3
 64 <211> LENGTH: 29
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Artificial Sequence

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68 <220> FEATURE:
69 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
72 <400> SEQUENCE: 3
73 tggtttcggt accgacaacc ttgtatccc 29
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 28
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE, 21968
83 <400> SEQUENCE: 4
84 gagttggtcc cagacagact ttgtcgt 28
86 <210> SEQ ID NO: 5
87 <211> LENGTH: 1389
88 <212> TYPE: DNA
89 <213> ORGANISM: Exophiala spinifera
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)...(1386)
95 <400> SEQUENCE: 5
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98 1 5 10 15
100 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
101 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
102 20 25 30
104 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
105 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
106 35 40 45
108 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
109 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
110 50 55 60
112 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
113 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
114 65 70 75 80
116 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
117 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
118 85 90 95
120 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
121 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
122 100 105 110
124 gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384
125 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
126 115 120 125
128 gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432
129 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 130 135 140
132 ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480
133 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu

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134	145	150	155	160	
136	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt				528
137	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly				
138		165	170	175	
140	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag				576
141	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys				
142		180	185	190	
144	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg				624
145	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly				
146		195	200	205	
148	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg				672
149	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met				
150		210	215	220	
152	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct				720
153	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala				
154	225	230	235	240	
156	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc				768
157	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly				
158		245	250	255	
160	gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg				816
161	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu				
162		260	265	270	
164	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca				864
165	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala				
166		275	280	285	
168	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta				912
169	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val				
170		290	295	300	
172	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa				960
173	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln				
174	305	310	315	320	
176	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc				1008
177	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val				
178		325	330	335	
180	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg				1056
181	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg				
182		340	345	350	
184	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac				1104
185	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp				
186		355	360	365	
188	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg				1152
189	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro				
190		370	375	380	
192	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga				1200
193	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly				
194	385	390	395	400	
196	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg				1248
197	Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser				
198		405	410	415	

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200 gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
201 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
202          420          425          430
204 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
205 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
206          435          440          445
208 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca      1386
209 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
210          450          455          460
212 tag      1389
214 <210> SEQ ID NO: 6
215 <211> LENGTH: 462
216 <212> TYPE: PRT
217 <213> ORGANISM: Exophiala spinifera
219 <400> SEQUENCE: 6
220 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
221 1          5          10          15
222 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
223          20          25          30
224 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
225          35          40          45
226 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
227          50          55          60
228 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
229 65          70          75          80
230 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
231          85          90          95
232 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
233          100          105          110
234 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
235          115          120          125
236 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
237          130          135          140
238 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
239 145          150          155          160
240 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
241          165          170          175
242 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
243          180          185          190
244 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
245          195          200          205
246 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
247          210          215          220
248 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
249 225          230          235          240
250 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
251          245          250          255
252 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
253          260          265          270

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254 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
255           275           280           285
256 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
257       290           295           300
258 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
259 305           310           315           320
260 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
261           325           330           335
262 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
263           340           345           350
264 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
265           355           360           365
266 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
267       370           375           380
268 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
269 385           390           395           400
270 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
271           405           410           415
272 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
273           420           425           430
274 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
275       435           440           445
276 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
277       450           455           460
279 <210> SEQ ID NO: 7
280 <211> LENGTH: 1442
281 <212> TYPE: DNA
282 <213> ORGANISM: Exophiala spinifera
284 <220> FEATURE:
285 <221> NAME/KEY: CDS
286 <222> LOCATION: (1)...(646)
288 <221> NAME/KEY: intron
289 <222> LOCATION: (647)...(699)
291 <221> NAME/KEY: CDS
292 <222> LOCATION: (700)...(1439)
294 <400> SEQUENCE: 7
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296 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
297 1           5           10           15
299 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
300 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
301           20           25           30
303 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
304 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
305           35           40           45
307 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
308 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
309       50           55           60
311 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag      240

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Please Note:

Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequenc which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:352 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1340 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1341 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3173 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3174 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:4214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:4275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40